1. An oligonucleotide primer, wherein said primer is capable of specifically hybridizing to a DNA having the sequence of the flanking regions of a microsatellite selected from the group consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21, M2_2_22, M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32, M2_4_33, M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48.

2. The oligonucleotide primer according to claim 1, wherein the sequence of said primer is selected from the group consisting of SEQ ID NOs: 1-42.

3. A kit for determining the number of repeat units of a microsatellite selected from the group consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21, M2_2_22, M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32, M2_4_33, M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48, the kit comprising a pair of oligonucleotide primers having the sequence of the flanking regions of said microsatellite.

4. The kit according to claim 3, wherein the pair of oligonucleotide primers is selected from the group consisting of
(a) SEQ ID NO: 1 and SEQ ID NO: 2,
(b) SEQ ID NO: 3 and SEQ ID NO: 4,
(c) SEQ ID NO: 5 and SEQ ID NO: 6,
(d) SEQ ID NO: 7 and SEQ ID NO: 8,
(e) SEQ ID NO: 9 and SEQ ID NO: 10,
(f) SEQ ID NO: 11 and SEQ ID NO: 12,
(g) SEQ ID NO: 13 and SEQ ID NO: 14,
(h) SEQ ID NO: 15 and SEQ ID NO: 16,
(i) SEQ ID NO: 17 and SEQ ID NO: 18,
(j) SEQ ID NO: 19 and SEQ ID NO: 20,
(k) SEQ ID NO: 21 and SEQ ID NO: 22,
(l) SEQ ID NO: 23 and SEQ ID NO: 24,
(m) SEQ ID NO: 25 and SEQ ID NO: 26,

(n) SEQ ID NO: 27 and SEQ ID NO: 28,
(o) SEQ ID NO: 29 and SEQ ID NO: 30,
(p) SEQ ID NO: 31 and SEQ ID NO: 32,
(q) SEQ ID NO: 33 and SEQ ID NO: 34,
(r) SEQ ID NO: 35 and SEQ ID NO: 36,
(s) SEQ ID NO: 37 and SEQ ID NO: 38,
(t) SEQ ID NO: 39 and SEQ ID NO: 40, and
(u) SEQ ID NO: 41 and SEQ ID NO: 42.

5. A method for determining the number of repeat units of a microsatellite, the method comprising a step for determining the number of repeat units in the region of which DNA can be amplified by using a pair of oligonucleotide primers selected from the group consisting of,
(a) SEQ ID NO: 1 and SEQ ID NO: 2,
(b) SEQ ID NO: 3 and SEQ ID NO: 4,
(c) SEQ ID NO: 5 and SEQ ID NO: 6,
(d) SEQ ID NO: 7 and SEQ ID NO: 8,
(e) SEQ ID NO: 9 and SEQ ID NO: 10,
(f) SEQ ID NO: 11 and SEQ ID NO: 12,
(g) SEQ ID NO: 13 and SEQ ID NO: 14,
(h) SEQ ID NO: 15 and SEQ ID NO: 16,
(i) SEQ ID NO: 17 and SEQ ID NO: 18,
(j) SEQ ID NO: 19 and SEQ ID NO: 20,
(k) SEQ ID NO: 21 and SEQ ID NO: 22,
(l) SEQ ID NO: 23 and SEQ ID NO: 24,
(m) SEQ ID NO: 25 and SEQ ID NO: 26,
(n) SEQ ID NO: 27 and SEQ ID NO: 28,
(o) SEQ ID NO: 29 and SEQ ID NO: 30,
(p) SEQ ID NO: 31 and SEQ ID NO: 32,
(q) SEQ ID NO: 33 and SEQ ID NO: 34,
(r) SEQ ID NO: 35 and SEQ ID NO: 36,
(s) SEQ ID NO: 37 and SEQ ID NO: 38,

(t) SEQ ID NO: 39 and SEQ ID NO: 40, and

(u) SEQ ID NO: 41 and SEQ ID NO: 42.

6. A method for mapping of susceptibility genes for disease associated with HLA class II alleles, by using a microsatellite marker selected from the group consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21, M2_2_22, M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32, M2_4_33, M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48, the method comprising:
(a) determining the number of repeat units of said microsatellite,
(b) estimating the allele frequencies of patients and controls, based on said number, and
(c) comparing the allele frequencies of patients with those of controls.

7. The method according to claim 6, the method comprising:
(a) amplifying a region of microsatellite using the oligonucleotide primer capable of selectively hybridizing to a DNA having a sequence of flanking regions of said microsatellite,
(b) determining the number of repeat units of said microsatellite,
(c) estimating the allele frequencies of patients and controls, based on the number, and
(d) comparing the allele frequencies of patients with those of controls.

8. A method for genotyping of a microsatellite allele selected from the group consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21, M2_2_22, M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32, M2_4_33, M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48, the method comprising:
(a) amplifying a region of the microsatellite, and
(b) determining the number of repeat units of said microsatellite.

9. The method according to claim 7, wherein said amplifying is performed by using the oligonucleotide primer selected from the group consisting of SEQ ID NOs: 1-42.